

December 21 2007--0275543 sequence listing\_ST25.txt  
SEQUENCE LISTING

<110> Hanna, Nabil  
Newman, Roland A.  
Reff, Mitchell E.

<120> Recombinant Anti-CD4 Antibodies for Human Therapy

<130> 037003-0275543

<140> 09/612,914

<141> 2000-07-10

<150> 08/523,894

<151> 1995-09-06

<150> 08/476,237

<151> 1995-06-07

<160> 59

<170> PatentIn version 3.4

<210> 1

<211> 423

<212> DNA

<213> Monkey

<220>

<221> misc\_feature

<222> (4)..(423)

<223> Heavy chain variable domain of CE9.1

<220>

<221> CDS

<222> (4)..(423)

<220>

<221> mat\_peptide

<222> (61)..(423)

<400> 1

gac atg aaa cac ctg tgg ttc ttc ctc ctc ctg gtg gca gcc ccc aga	48
Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg	
-15 -10 -5	

tgg gtc ttg tcc cag gtg cag ctg cag gag gcg ggc cca gga ctg gtg	96
Trp Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val	
-1 1 5 10	

aag cct tgc gag acc ctg tcc ctc acc tgc agt gtc tct ggt ggc tcc	144
Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser	
15 20 25	

atc agc ggt gac tat tat tgg ttc tgg atc cgc cag tcc cca ggg aag	192
Ile Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys	
30 35 40	

gga ctg gag tgg atc ggc tac atc tat ggc agt ggt ggg ggc acc aat	240
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn	
45 50 55 60	

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tac aat ccc tcc ctc aac aat cga gtc tcc att tca ata gac acg tcc 288  
Tyr Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser  
65 70 75

aag aac ctc ttc tcc ctg aaa ctg agg tct gtg acc gcc gcg gac acg 336  
Lys Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr  
80 85 90

gcc gtc tat tac tgt gcg agt aat ata ttg aaa tat ctt cac tgg tta 384  
Ala Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu  
95 100 105

tta tac tgg ggc cag gga gtc ctg gtc acc gtc tcc tca 423  
Leu Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

<210> 2  
<211> 140  
<212> PRT  
<213> Monkey

<400> 2

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
-15 -10 -5

Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val Lys  
-1 1 5 10

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile  
15 20 25

Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly  
30 35 40 45

Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr  
50 55 60

Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
65 70 75

Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
80 85 90

Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
95 100 105

Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser  
110 115 120

<210> 3  
<211> 387  
<212> DNA

&lt;213&gt; Monkey

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (4)..(387)

&lt;223&gt; Light chain variable domain of CD9.1

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (4)..(387)

&lt;220&gt;

&lt;221&gt; mat\_peptide

&lt;222&gt; (61)..(387)

&lt;400&gt; 3

```
acc atg gcc tgg gct ctg ctg ctc ctc ggc ctc ctt gct cac ttt aca      48
   Met Ala Trp Ala Leu Leu Leu Gly Leu Ala His Phe Thr
                        -15                      -10                      -5
```

```
gac tct gcg gcc tcc tat gag ttg agt cag cct cgc tca gtg tcc gtg      96
Asp Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val
                        -1      1                      5                      10
```

```
tcc cca gga cag acg gcc ggg ttc acc tgt ggg gga gac aac gtt gga      144
Ser Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly
                        15                      20                      25
```

```
agg aaa agt gta cag tgg tac cag cag aag cca ccg cag gcc cct gtg      192
Arg Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val
                        30                      35                      40
```

```
ctg gtc atc tat gct gac agc gaa cgg ccc tca ggg atc cct gcg cga      240
Leu Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg
45                      50                      55                      60
```

```
ttc tct ggc tcc aac tca ggg aac acc gcc acc ctg acc atc agc ggg      288
Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
                        65                      70                      75
```

```
gtc gag gcc ggg gat gag gct gac tat tac tgt cag gtg tgg gac agt      336
Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser
                        80                      85                      90
```

```
act gct gat cat tgg gtc ttc ggc gga ggg acc cgg ctg acc gtc cta      384
Thr Ala Asp His Trp Val Phe Gly Gly Thr Arg Leu Thr Val Leu
                        95                      100                      105
```

```
ggg      387
Gly
```

&lt;210&gt; 4

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Monkey

&lt;400&gt; 4

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Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp
                        -15                      -10                      -5
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Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser  
 -1 1 5 10

Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg  
 15 20 25

Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu  
 30 35 40 45

Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe  
 50 55 60

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val  
 65 70 75

Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr  
 80 85 90

Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly  
 95 100 105

<210> 5  
 <211> 702  
 <212> DNA  
 <213> Human or Monkey

<220>  
 <221> misc\_feature  
 <222> (1)..(702)  
 <223> Lambda variable and constant domains in CE9.1

<220>  
 <221> CDS  
 <222> (1)..(702)

<400> 5  
 atg gcc tgg gct ctg ctg ctc ctc ggc ctc ctt gct cac ttt aca gac 48  
 Met Ala Trp Ala Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp  
 1 5 10 15

tct gcg gcc tcc tat gag ttg agt cag cct cgc tca gtg tcc gtg tcc 96  
 Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser  
 20 25 30

cca gga cag acg gcc ggg ttc acc tgt ggg gga gac aac gtt gga agg 144  
 Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg  
 35 40 45

aaa agt gta cag tgg tac cag cag aag cca ccg cag gcc cct gtg ctg 192  
 Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu  
 50 55 60

gtc atc tat gct gac agc gaa cgg ccc tca ggg atc cct gcg cga ttc 240  
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```

val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe
65                               70                               75
tct ggc tcc aac tca ggg aac acc gcc acc ctg acc atc agc ggg gtc      288
Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val
85                               90                               95
gag gcc ggg gat gag gct gac tat tac tgt cag gtg tgg gac agt act      336
Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr
100                              105                              110
gct gat cat tgg gtc ttc ggc gga ggg acc cgg ctg acc gtc cta ggt      384
Ala Asp His Trp Val Phe Gly Gly Thr Arg Leu Thr Val Leu Gly
115                              120                              125
cag ccc aag gct gcc ccc tcg gtc act ctg ttc cgg ccc tcc tct gag      432
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Ser Ser Glu
130                              135                              140
gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc      480
Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
145                              150                              155
tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc      528
Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Val
165                              170                              175
aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag      576
Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
180                              185                              190
tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag tcc      624
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
195                              200                              205
cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag      672
His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
210                              215                              220
aag aca gtg gcc cct aca gaa tgt tca tga      702
Lys Thr Val Ala Pro Thr Glu Cys Ser
225                              230

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<210> 6
<211> 233
<212> PRT
<213> Human or Monkey

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<400> 6

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Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp
1                               5                               10                               15
Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser
20                              25                              30
Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg
35                              40                              45

```

Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu  
50 55 60

Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe  
65 70 75 80

Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val  
85 90 95

Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr  
100 105 110

Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly  
115 120 125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
130 135 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
145 150 155 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
165 170 175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
180 185 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
195 200 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
210 215 220

Lys Thr Val Ala Pro Thr Glu Cys Ser  
225 230

<210> 7  
<211> 1404  
<212> DNA  
<213> Human or Monkey

<220>  
<221> misc\_feature  
<222> (1)..(1404)  
<223> Heavy chain variable and constant gamma 4

<220>  
<221> CDS  
<222> (1)..(1404)

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<400> 7  
 atg aaa cac ctg tgg ttc ttc ctc ctc ctg gtg gca gcc ccc aga tgg 48  
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

gtc ttg tcc cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag 96  
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
 20 25 30

cct tcg gag acc ctg tcc ctc acc tgc agt gtc tct ggt ggc tcc atc 144  
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile  
 35 40 45

agc ggt gac tat tat tgg ttc tgg atc cgc cag tcc cca ggg aag gga 192  
 Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly  
 50 55 60

ctg gag tgg atc ggc tac atc tat ggc agt ggt ggc ggc acc aat tac 240  
 Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Thr Asn Tyr  
 65 70 75 80

aat ccc tcc ctc aac aat cga gtc tcc att tca ata gac acg tcc aag 288  
 Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
 85 90 95

aac ctc ttc tcc ctg aaa ctg agg tct gtg acc gcc gcg gac acg gcc 336  
 Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
 100 105 110

gtc tat tac tgt gcg agt aat ata ttg aaa tat ctt cac tgg tta tta 384  
 Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
 115 120 125

tac tgg ggc cag gga gtc ctg gtc acc gtc tcc tca gct agc acc aag 432  
 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
 130 135 140

ggc cca tcc gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag 480  
 Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
 145 150 155 160

agc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg 528  
 Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 165 170 175

gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc 576  
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 180 185 190

ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg 624  
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 195 200 205

gtg acc gtg ccc tcc agc agc ttg ggc acg aag acc tac acc tgc aac 672  
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
 210 215 220

gta gat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag tcc 720  
 Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
 225 230 235 240

aaa tat ggt ccc cca tgc cca tca tgc cca gca cct gag ttc ctg ggg 768  
 Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly  
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245 250 255

gga cca tca gtc ttc ctg ttc ccc cca aaa ccc aag gac act ctc atg Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met	816
atc tcc cgg acc cct gag gtc acg tgc gtg gtg gtg gac gtg agc cag Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln	864
gaa gac ccc gag gtc cag ttc aac tgg tac gtg gat ggc gtg gag gtg Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val	912
cat aat gcc aag aca aag ccg cgg gag gag cag ttc aac agc acg tac His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr	960
cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aac ggc Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	1008
aag gag tac aag tgc aag gtc tcc aac aaa ggc ctc ccg tcc tcc atc Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile	1056
gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gag cca cag gtg Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val	1104
tac acc ctg ccc cca tcc cag gag gag atg acc aag aac cag gtc agc Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser	1152
ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu	1200
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro	1248
gtg ctg gac tcc gac ggc tcc ttc ttc ctg tac agc agg cta acc gtg Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val	1296
gac aag agc agg tgg cag gag ggg aat gtc ttc tca tgc tcc gtg atg Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met	1344
cat gag gct ctg cac aac cac tac aca cag aag agc ctc tcc ctg tct His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	1392
ctg ggt aaa tga Leu Gly Lys	1404

<210> 8  
<211> 467  
<212> PRT  
<213> Human or Monkey



&lt;400&gt; 8

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
 20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile  
 35 40 45

Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly  
 50 55 60

Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr  
 65 70 75 80

Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
 85 90 95

Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
 100 105 110

Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
 115 120 125

Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
 130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
 145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
 210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
 225 230 235 240

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Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly  
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

Leu Gly Lys  
465

<210> 9  
<211> 1404  
<212> DNA

&lt;213&gt; Human or Monkey

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1404)

&lt;223&gt; Heavy chain gamma 4 with the E mutation

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1404)

&lt;400&gt; 9

atg	aaa	cac	ctg	tgg	ttc	ttc	ctc	ctc	ctg	gtg	gca	gcc	ccc	aga	tgg	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Val	Ala	Ala	Pro	Arg	Trp		
1			5					10					15			

gtc	tgt	tcc	cag	gtg	cag	ctg	cag	gag	tgc	ggc	cca	gga	ctg	gtg	aag	96
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	
			20					25					30			

cct	tgc	gag	acc	ctg	tcc	ctc	acc	tgc	agt	gtc	tct	ggc	ggc	tcc	atc	144
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Gly	Ser	Ile	
			35				40					45				

agc	ggc	gac	tat	tat	tgg	ttc	tgg	atc	cgc	cag	tcc	cca	ggg	aag	gga	192
Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	
	50					55					60					

ctg	gag	tgg	atc	ggc	tac	atc	tat	ggc	agt	ggc	ggg	ggc	acc	aat	tac	240
Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	Tyr	
	65				70			75						80		

aat	ccc	tcc	ctc	aac	aat	cga	gtc	tcc	att	tca	ata	gac	acg	tcc	aag	288
Asn	Pro	Ser	Leu	Asn	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	Lys	
				85				90						95		

aac	ctc	ttc	tcc	ctg	aaa	ctg	agg	tct	gtg	acc	gcc	gcg	gac	acg	gcc	336
Asn	Leu	Phe	Ser	Leu	Lys	Leu	Arg	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	
			100					105					110			

gtc	tat	tac	tgt	gcg	agt	aat	ata	ttg	aaa	tat	ctt	cac	tgg	tta	tta	384
Val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu	His	Trp	Leu	Leu	
			115				120					125				

tac	tgg	ggc	cag	gga	gtc	ctg	gtc	acc	gtc	tcc	tca	gct	agc	acc	aag	432
Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser	Ala	Ala	Ser	Thr	Lys	
	130					135					140					

ggg	cca	tcc	gtc	ttc	ccc	ctg	gcg	ccc	tgc	tcc	agg	agc	acc	tcc	gag	480
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	
	145				150				155						160	

agc	aca	gcc	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	528
Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	
				165					170					175		

gtg	acg	gtg	tgc	tgg	aac	tca	ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	576
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	
				180				185					190			

ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	624
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	

## December 21 2007--0275543 sequence\_listing\_ST25.txt

195	gtg acc gtc ccc tcc agc agc ttg ggc acg aag acc tac acc tgc aac	672
	Val Thr Val Pro Ser Ser 215 Leu Gly Thr Lys 220 Tyr Thr Cys Asn	
225	gta gat cac aag ccc agc aac acc aag gtc gac aag aga gtt gag tcc	720
	Val Asp His Lys Pro Ser 230 Asn Thr Lys Val Asp 235 Lys Arg Val Glu Ser 240	
768	aaa tat ggt ccc cca tgc cca tca tgc cca gca cct gag ttc gag ggg	
	Lys Tyr Gly Pro 245 Pro Cys Pro Ser Cys 250 Ala Pro Glu Phe 255 Glu Gly	
816	gga cca tca gtc ttc ctg ttc ccc cca aaa ccc aag gac act ctc atg	
	Gly Pro Ser Val 260 Phe Leu Phe Pro 265 Pro Lys Pro Lys Asp Thr 270 Leu Met	
864	atc tcc cgg acc cct gag gtc acg tgc gtc gtc gtc gac gtc agc cag	
	Ile Ser 275 Arg Thr Pro Glu Val Thr 280 Cys Val Val Val Asp 285 Val Ser Gln	
912	gaa gac ccc gag gtc cag ttc aac tgg tac gtc gat ggc gtc gag gtc	
	Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp 300 Gly Val Glu Val	
960	cat aat gcc aag aca aag ccg cgg gag gag cag ttc aac agc acg tac	
	His Asn Ala Lys Thr Lys 310 Pro Arg Glu Glu 315 Phe Asn Ser Thr 320	
1008	cgt gtc gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aac ggc	
	Arg Val Val Ser Val 325 Leu Thr Val Leu His 330 Gln Asp Trp Leu Asn Gly 335	
1056	aag gag tac aag tgc aag gtc tcc aac aaa ggc ctc ccg tcc tcc atc	
	Lys Glu Tyr Lys 340 Cys Lys Val Ser Asn Lys 345 Gly Leu Pro Ser 350 Ser Ile	
1104	gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gag cca cag gtc	
	Glu Lys Thr Ile Ser Lys Ala Lys 360 Gly Gln Pro Arg Glu Pro Gln Val	
1152	tac acc ctg ccc cca tcc cag gag gag atg acc aag aac cag gtc agc	
	Tyr Thr 370 Leu Pro Pro Ser Gln Glu Glu Met Thr Lys 380 Asn Gln Val Ser	
1200	ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtc gag	
	Leu Thr Cys Leu Val Lys 390 Gly Phe Tyr Pro 395 Asp Ile Ala Val Glu 400	
1248	tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc	
	Trp Glu Ser Asn 405 Gln Pro Glu Asn Asn 410 Tyr Lys Thr Thr 415 Pro Pro	
1296	gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc agg cta acc gtc	
	Val Leu Asp 420 Ser Asp Gly Ser Phe 425 Leu Tyr Ser Arg 430 Thr Val	
1344	gac aag agc agg tgg cag gag ggg aat gtc ttc tca tgc tcc gtc atg	
	Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser 445 Cys Ser Val Met	
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 Leu Gly Lys  
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1404

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 20 25 30

Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Ser Ile  
 35 40 45

Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly  
 50 55 60

Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr  
 65 70 75 80

Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
 85 90 95

Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
 100 105 110

Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
 115 120 125

Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
 130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
 145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
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Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
225 230 235 240

Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Glu Gly  
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
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Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
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His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
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Leu Gly Lys  
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gtc ttg tcc cag gtg cag ctg cag gag tgc ggc cca gga ctg gtg aag 96  
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
20 25 30

cct tcg gag acc ctg tcc ctc acc tgc agt gtc tct ggt ggc tcc atc 144  
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile  
35 40 45

agc ggt gac tat tat tgg ttc tgg atc cgc cag tcc cca ggg aag gga 192  
Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly  
50 55 60

ctg gag tgg atc ggc tac atc tat ggc agt ggt ggg ggc acc aat tac 240  
Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr  
65 70 75 80

aat ccc tcc ctc aac aat cga gtc tcc att tca ata gac acg tcc aag 288  
Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
85 90 95

aac ctc ttc tcc ctg aaa ctg agg tct gtg acc gcc gcg gac acg gcc 336  
Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
100 105 110

gtc tat tac tgt gcg agt aat ata ttg aaa tat ctt cac tgg tta tta 384  
Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
115 120 125

tac tgg ggc cag gga gtc ctg gtc acc gtc tcc tca gct agc acc aag 432  
Tyr Trp Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

ggg cca tcc gtc ttc ccc ctg gcg ccc tgc tcc agg agc acc tcc gag 480  
Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
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145		150		155		160	
agc aca gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg	528						
Ser Thr Ala Ala Leu 165				Lys 170	Asp Tyr Phe Pro Glu Pro		
gtg acg gtg tgc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc	576						
Val Thr Val Ser 180				Ala 185	Leu Thr Ser Gly Val His Thr		
ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg	624						
Phe Pro 195				Ser 200	Gly Leu Tyr Ser Leu Ser Ser Val		
gtg acc gtg ccc tcc agc agc ttg ggc acg aag acc tac acc tgc aac	672						
Val Thr 210				Leu 215	Gly Thr Lys Thr Tyr Thr Cys Asn		
gta gat cac aag ccc agc aac acc aag gtg gac aag aga gtt gag tcc	720						
Val Asp His Lys Pro 230				Thr 235	Asp Lys Arg Val Glu Ser 240		
aaa tat ggt ccc cca tgc cca cca tgc cca gca cct gag ttc gag ggg	768						
Lys Tyr Gly Pro 245				Cys Pro 250	Ala Pro Glu Phe Glu Gly 255		
gga cca tca gtc ttc ctg ttc ccc cca aaa ccc aag gac act ctc atg	816						
Gly Pro Ser Val 260				Phe 265	Pro Lys Pro Lys Asp Thr 270		
atc tcc cgg acc cct gag gtc acg tgc gtg gtg gtg gac gtg agc cag	864						
Ile Ser Arg Thr 275				Thr 280	Cys Val Val Val Asp Val Ser Gln		
gaa gac ccc gag gtc cag ttc aac tgg tac gtg gat ggc gtg gag gtg	912						
Glu Asp Pro Glu Val Gln 295				Asn Trp Tyr Val Asp 300	Gly Val Glu Val		
cat aat gcc aag aca aag cgg gag gag cag aac agc acg tac	960						
His Asn Ala Lys Thr 310				Arg Glu Glu Gln Phe Asn Ser Thr Tyr 320			
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Arg Val Val Ser 325				Thr Val Leu His 330	Gln Asp Trp Leu Asn Gly 335		
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Lys Glu Tyr 340				Asn Lys 345	Gly Leu Pro 350	Ser Ser Ile	
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Glu Lys Thr Ile 355				Ala Lys 360	Gly Gln Pro Arg 365	Pro Gln Val	
tac acc ctg ccc cca tcc cag gag gag atg acc aag aac cag gtc agc	1152						
Tyr Thr Leu Pro 370				Gln Glu 375	Met Thr Lys 380	Asn Gln Val Ser	
ctg acc tgc ctg gtc aaa ggc ttc tac ccc agc gac atc gcc gtg gag	1200						
Leu Thr Cys Leu Val 390				Gly Phe Tyr Pro 395	Asp Ile Ala Val Glu 400		
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc	1248						



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Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro		
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gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	agg	cta	acc	gtg	1296
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	
			420					425					430			
gac	aag	agc	agg	tgg	cag	gag	ggg	aat	gtc	ttc	tca	tgc	tcc	gtg	atg	1344
Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
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cat	gag	gct	ctg	cac	aac	cac	tac	aca	cag	aag	agc	ctc	tcc	ctg	tct	1392
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
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Leu	Gly	Lys														
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			20					25					30			
Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	val	Ser	Gly	Gly	Ser	Ile	
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Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	
	50					55					60					
Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	Tyr	
65					70				75					80		
Asn	Pro	Ser	Leu	Asn	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	Lys	
			85					90						95		
Asn	Leu	Phe	Ser	Leu	Lys	Leu	Arg	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	
		100						105					110			
val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu	His	Trp	Leu	Leu	
		115					120					125				
Tyr	Trp	Gly	Gln	Gly	val	Leu	val	Thr	val	Ser	Ser	Ala	Ser	Thr	Lys	
	130					135					140					

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Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
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Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
225 230 235 240

Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly  
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

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Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
450 455 460

Leu Gly Lys  
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<223> Lambda light chain primer with AvrII site

<400> 43
cttgggctga cctaggacgg tcagccg
27

<210> 44
<211> 17
<212> DNA
<213> Human or Monkey

<220>
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<223> VH1 heavy chain variable region

<400> 44
ccatggactg gacctgg
17

<210> 45
<211> 20
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<213> Human or Monkey

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<223> VH2 heavy chain variable region

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<210> 46
<211> 20
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<223> VH3 heavy chain variable region

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<400> 46  
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<210> 47  
<211> 20  
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<210> 48  
<211> 20  
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<210> 49  
<211> 20  
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<220>  
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<400> 49  
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<210> 50  
<211> 16  
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<220>  
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<400> 50  
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<210> 51  
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<220>  
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<400> 51  
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<210> 52  
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<220>  
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<400> 52  
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<210> 53  
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<220>  
 <221> misc\_feature  
 <222> (5)..(5)  
 <223> n is C or T

<220>  
 <221> misc\_feature  
 <222> (7)..(7)  
 <223> n is T or C

<220>  
 <221> misc\_feature  
 <222> (8)..(8)  
 <223> n is G or A

<220>

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<221> misc_feature
<222> (13)..(13)
<223> n is A or C

<400> 53
ctcantnnct gcncagggtc c                                21

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<212> DNA
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<220>
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<223> Kappa light chain constant region

<400> 54
aagacagatg gtgcagcca                                19

<210> 55
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<212> DNA
<213> Human or Monkey

<220>
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<400> 55
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<210> 56
<211> 30
<212> DNA
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<220>
<221> misc_feature
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<223> PCR primer for Human gamma 4 constant region

<400> 56
gggggatcc tcatttacc agagacaggg                        30

<210> 57
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<212> DNA
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<220>
<221> misc_feature
<222> (1)..(31)
<223> PCR primer for Human gamma 4 constant region

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<400> 57
gggggctagc accaagggcc catccgtctt c 31

<210> 58
<211> 96
<212> DNA
<213> Human or Monkey

<220>
<221> misc_feature
<222> (1)..(96)
<223> PCR mutagenesis of human gamma 4

<400> 58
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ctcgaactca ggtgctgggc atggtgggca tggggg 96

<210> 59
<211> 27
<212> DNA
<213> Human or Monkey

<220>
<221> misc_feature
<222> (1)..(27)
<223> PCR mutagenesis of human gamma 4

<400> 59
tcctcagcta gcaccaagg gccatcc 27

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